What is claimed is:

- 1. A method for identifying bioactivities or biomolecules using high throughput creening of nucleic acid comprising:
 - providing a gene library containing a plurality of clones, wherein the DNA for generating the library is obtained from more than one organism;
 - b) encapsulating a bioactive substrate and at least one clone of the library in a gel microdroplet, wherein a bioactivity or biomolecule produced by the clone is detectable by a difference in the substrate prior to contacting with the at least one clone as compared to after contacting;
 - c) screening the microdroplet with an assay or an analyzer that detects a bioactivity or biomolecule; and
 - d) identifying clones detected as positive for a change in the substrate, wherein a change in the substrate is indicative of DNA that encodes a bioactivity or biomolecule.
- 2. The method of claim 1, wherein the bioactivity is provided by an enzyme is selected from the group consisting of lipases, esterases, proteases, glycosidases, glycosyl transferases, phosphatases, kinases, mono- and dioxygenases, haloperoxidases, lignin peroxidases, diarylpropane peroxidases, epozide hydrolases, nitrile hydratases, nitrilases, transaminases, amidases, and acylases.
 - 3. The method of claim 1, wherein the library is generated in a prokaryotic cell.
- 4. The method of claim 1, wherein the library is generated in a Streptomyces sp.
- 5. The method of claim 4, wherein the Streptomyces is Streptomyces venezuelae.
- 6. The method of claim 3, wherein the prokaryotic cell is gram negative.

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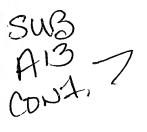
- 7. The method of claim 1, wherein the gene library is an expression library.
- 8. The method of claim 5, wherein the expression library contains DNA obtained from extremophiles.
- 9. The method of claim 8, wherein the extremophiles are thermophiles.

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- 10. The method of claim 9, wherein the extremeophiles are selected from the group consisting of hyperthermophiles, psychrophiles, halophiles, psychrotrophs, alkalophiles, and acidophiles.
- 11. The method of claim 1, wherein the bioactive substrate comprises C12FDG.
- 12. The method of claim 1, wherein the bioactive substrate comprises a lipophilic tail.
- 13. The method of claim 1, wherein the the samples are heated before step b).
- 14. The method of claim 13, wherein the heating is at about 70°C.
- 15. The method of claim 14, wherein the heating occurs at about 30 minutes.
- 16. The method of claim 1, wherein the analyzer comprises a fluorescent analyzer.
- 17. The method of claim 16, wherein the fluorescent analyzer is a FACS apparatus.
- 18. The method of claim 1, wherein the library is biopanned before step b).
- 19. The method of claim 4, wherein the prokaryotic cell is *E. coli*.

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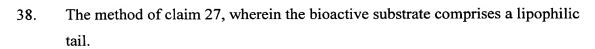
- 20. The method of claim 19, wherein prior to step b), the *E. coli* is transferred to a *Streptomyces* sp.
- 21. The method of claim 20, wherein the *Streptomyces* sp. is *Streptomyces* venezuelae.
- 22. The method of claim 1, wherein the library is normalized before step b).
- 23. The method of claim 1, further comprising co-encapsulating an indicator cell in step b).
- 24. The method of claim 1, wherein the analyzer is a chromogenic analyzer.
- 25. The method of claim 1, wherein the assay is an immunoassay.
- 26. A method for identifying bioactivities or biomolecules using high throughput screening of nucleic acid comprising:
 - a) providing a gene library containing a plurality of clones, wherein the nucleic acid for generating the library is obtained from more than one organism;
 - b) inserting a bioactive substrate into the clones of the library, wherein a change in the substrate is detectable in the presence of a bioactivity or biomolecule;
 - c) screening the clones with an assay of an analyzer that detects the presence of a bioactivity or a biomolecule; and
 - d) identifying clones detected as positive for a change in the substrate, wherein a change in the substrate is indicative of DNA that encodes a bioactivity or biomolecule.

27. The method of claim 26, further comprising encapsulation the clone and the bioactive substrate prior to screening.

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- The method of claim 27, wherein the bioactivity is provided by an enzyme is selected from the group consisting of lipases, esterases, proteases, glycosidases, glycosyl transferases, phosphatases, kinases, mono- and dioxygenases, haloperoxidases, lignin peroxidases, diarylpropane peroxidases, epozide hydrolases, nitrile hydratases, mitrilases, transaminases, amidases, and acylases.
- 29. The method of claim 27, wherein the library is generated in a prokaryotic cell.
- 30. The method of claim 27, wherein the library is generated in a Streptomyces sp.
- 31. The method of claim 30, wherein the Streptomyces is Streptomyces venezuelae.
- 32. The method of claim 29, wherein the prokaryotic cell is gram negative.
- 33. The method of claim 27, wherein the gene library is an expression library.
- 34. The method of claim 31, wherein the expression library contains DNA obtained from extremophiles.
- 35. The method of claim 34, wherein the extremophiles are thermophiles.
- 36. The method of claim 35, wherein the extremeophiles are selected from the group consisting of hyperthermophiles, psychrophiles, halophiles, psychrotrophs, alkalophiles, and acadophiles.
- 37. The method of claim 27, wherein the bioactive substrate comprises C12FDG.



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- 39. The method of claim 27, wherein the the samples are heated before step b).
- 40. The method of claim 39, wherein the heating is at about 70°C.
- 41. The method of claim 40, wherein the heating occurs at about 30 minutes.
- 42. The method of claim 27, wherein the analyzer comprises a fluorescent analyzer.
- 43. The method of claim 42, wherein the fluorescent analyzer is a FACS apparatus.
- 44. The method of claim 27, wherein the library is biopanned before step b).
- 45. The method of claim 29, wherein the prokaryotic cell is *E. coli*.
- 46. The method of claim 45, wherein prior to step b), the *E. coli* is transferred to a myceliate bacteria or fungi.

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- 47. The method of claim 46, wherein the myceliate fungi is an *Actinomyces* sp.
- 48. The method of claim 46, wherein the myceliate bacteria is a Streptomyces sp.
- 49. The method of claim 47, wherein the *Streptomyces* sp. is *Streptomyces* venezuelae.

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50. The method of claim 27, wherein the library is normalized before step b).



- 51. The method of claim 27, further comprising co-encapsulating an indicator cell in step b).
- 52. The method of claim 27, wherein the analyzer is a chromogenic analyzer.
- 53. The method of claim 27, wherein the assay is an immunoassay.

